

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/773,977</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input checked="" type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

AMC/MH - Biotechnology Systems Branch - 08/21/2001

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/773,877

DATE: 08/07/2001
TIME: 08:23:37

Input Set : A:\REG 710B.txt
Output Set: N:\CRF3\08072001\I773877.raw

3 <110> APPLICANT: Xia, Yu-Ping et al.
 5 <120> TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
 7 <130> FILE REFERENCE: REG 710b
 9 <140> CURRENT APPLICATION NUMBER: 09/773,877
 10 <141> CURRENT FILING DATE: 2001-01-31
 12 <160> NUMBER OF SEQ ID NOS: 27
 14 <170> SOFTWARE: PatentIn version 3.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 36
 18 <212> TYPE: DNA
 C--> 19 <213> ORGANISM: Artificial ✓
 21 <220> FEATURE:
 22 <223> OTHER INFORMATION: Primer ✓
 24 <400> SEQUENCE: 1
 25 gactagcagt ccggaggttag acctttcgta gagatg 36
 28 <210> SEQ ID NO: 2
 29 <211> LENGTH: 33
 30 <212> TYPE: DNA
 C--> 31 <213> ORGANISM: Artificial ✓
 33 <220> FEATURE:
 34 <223> OTHER INFORMATION: Primer ✓
 36 <400> SEQUENCE: 2
 37 cggactcaga accacatcta tgattgtatt ggt 33
 40 <210> SEQ ID NO: 3
 41 <211> LENGTH: 35
 42 <212> TYPE: DNA
 C--> 43 <213> ORGANISM: Artificial ✓
 45 <220> FEATURE:
 46 <223> OTHER INFORMATION: Primer ✓
 48 <400> SEQUENCE: 3
 49 acaatcatag atgtggttct gagtccgtct catgg 35
 52 <210> SEQ ID NO: 4
 53 <211> LENGTH: 38
 54 <212> TYPE: DNA
 C--> 55 <213> ORGANISM: Artificial ✓
 57 <220> FEATURE:
 58 <223> OTHER INFORMATION: Primer ✓
 60 <400> SEQUENCE: 4
 61 gataatgccc gggccctttt catggaccct gacaaatg 38
 64 <210> SEQ ID NO: 5
 65 <211> LENGTH: 36
 66 <212> TYPE: DNA
 C--> 67 <213> ORGANISM: Artificial ✓
 69 <220> FEATURE:
 70 <223> OTHER INFORMATION: Primer ✓
 72 <400> SEQUENCE: 5
 73 gactagcagt ccggaggttag acctttcgta gagatg 36

Does Not Comply
Corrected Diskette Needed

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Input Set : A:\REG 710B.txt
Output Set: N:\CRF3\08072001\I773877.raw

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76 <210> SEQ ID NO: 6
77 <211> LENGTH: 38
78 <212> TYPE: DNA
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81 <220> FEATURE:
82 <223> OTHER INFORMATION: Primer
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85 ttcctggca acagctggat atctatgatt gtattggt 38
88 <210> SEQ ID NO: 7
89 <211> LENGTH: 39
90 <212> TYPE: DNA
C--> 91 <213> ORGANISM: Artificial
93 <220> FEATURE:
94 <223> OTHER INFORMATION: Primer
96 <400> SEQUENCE: 7
97 atccagctgt tgccaggaa gtcgctggag ctgctggta 39
100 <210> SEQ ID NO: 8
101 <211> LENGTH: 39
102 <212> TYPE: DNA
C--> 103 <213> ORGANISM: Artificial
105 <220> FEATURE:
106 <223> OTHER INFORMATION: Primer
108 <400> SEQUENCE: 8
109 attttcatgc acaatgaccc cggtgcttc ccgaaatcg 39
112 <210> SEQ ID NO: 9
113 <211> LENGTH: 38
114 <212> TYPE: DNA
C--> 115 <213> ORGANISM: Artificial
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Primer
120 <400> SEQUENCE: 9
121 tcatacatat ccagctgttg cccaggaagt cgctggag 38
124 <210> SEQ ID NO: 10
125 <211> LENGTH: 39
126 <212> TYPE: DNA
C--> 127 <213> ORGANISM: Artificial
129 <220> FEATURE:
130 <223> OTHER INFORMATION: Primer
132 <400> SEQUENCE: 10
133 gataatgccccc gggccatttt catgcacaat gacctcggt 39
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137 <211> LENGTH: 1704
138 <212> TYPE: DNA
C--> 139 <213> ORGANISM: Artificial
141 <220> FEATURE:
142 <223> OTHER INFORMATION: Flt1(1-3)-Fc
144 <220> FEATURE:
145 <221> NAME/KEY: CDS
146 <222> LOCATION: (1)..(1704)

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Input Set : A:\REG 710B.txt
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148 <400> SEQUENCE: 11		
149 atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg ctc agc	48	
150 Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser		
151 1 5 10 15		
153 tgt ctg ctt ctc aca gga tct agt tca ggt tca aaa tta aaa gat cct	96	
154 Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro		
155 20 25 30		
157 gaa ctg agt tta aaa ggc acc cag cac atc atg caa gca ggc cag aca	144	
158 Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr		
159 35 40 45		
161 ctg cat ctc caa tgc agg ggg gaa gca gcc cat aaa tgg tct ttg cct	192	
162 Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro		
163 50 55 60		
165 gaa atg gtg agt aag gaa agc gaa agg ctg agc ata act aaa tct gcc	240	
166 Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala		
167 65 70 75 80		
169 tgt gga aga aat ggc aaa caa ttc tgc agt act tta acc ttg aac aca	288	
170 Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr		
171 85 90 95		
173 gct caa gca aac cac act ggc ttc tac agc tgc aaa tat cta gct gta	336	
174 Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val		
175 100 105 110		
177 cct act tca aag aag gaa aca gaa tct gca atc tat ata ttt att	384	
178 Pro Thr Ser Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile		
179 115 120 125		
181 agt gat aca ggt aga cct ttc gta gag atg tac agt gaa atc ccc gaa	432	
182 Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu		
183 130 135 140		
185 att ata cac atg act gaa gga agg gag ctc gtc att ccc tgc cggt gtt	480	
186 Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val		
187 145 150 155 160		
189 acg tca cct aac atc act gtt act tta aaa aag ttt cca ctt gac act	528	
190 Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr		
191 165 170 175		
193 ttg atc cct gat gga aaa cgc ata atc tgg gac agt aga aag ggc ttc	576	
194 Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe		
195 180 185 190		
197 atc ata tca aat gca acg tac aaa gaa ata ggg ctt ctg acc tgt gaa	624	
198 Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu		
199 195 200 205		
201 gca aca gtc aat ggg cat ttg tat aag aca aac tat ctc aca cat cga	672	
202 Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg		
203 210 215 220		
205 caa acc aat aca atc ata gat gtc caa ata agc aca cca cgc cca gtc	720	
206 Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val		
207 225 230 235 240		
209 aaa tta ctt aga ggc cat act ctt gtc ctc aat tgt act gct acc act	768	
210 Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr		
211 245 250 255		

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213 ccc ttg aac acg aga gtt caa atg acc tgg agt tac cct gat gaa aaa	816
214 Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys	
215 260 265 270	
217 aat aag aga gct tcc gta agg cga cga att gac caa agc aat tcc cat	864
218 Asn Lys Arg Ala Ser Val Arg Arg Ile Asp Gln Ser Asn Ser His	
219 275 280 285	
221 gcc aac ata ttc tac agt gtt ctt act att gac aaa atg cag aac aaa	912
222 Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys	
223 290 295 300	
225 gac aaa gga ctt tat act tgt cgt gta agg agt gga cca tca ttc aaa	960
226 Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys	
227 305 310 315 320	
229 tct gtt aac acc tca gtg cat ata tat gat aaa gca ggc ccg ggc gag	1008
230 Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu	
231 325 330 335	
233 ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct	1056
234 Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro	
235 340 345 350	
237 gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag	1104
238 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys	
239 355 360 365	
241 gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg	1152
242 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val	
243 370 375 380	
245 gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac	1200
246 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp	
247 385 390 395 400	
249 ggc gtg gag gtg cat aat gcc aag aca aag ccg ccg gag gag cag tac	1248
250 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr	
251 405 410 415	
253 aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac	1296
254 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp	
255 420 425 430	
257 tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc	1344
258 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu	
259 435 440 445	
261 cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga	1392
262 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg	
263 450 455 460	
265 gaa cca cag gtg tac acc ctg ccc cca tcc ccg gat gag ctg acc aag	1440
266 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys	
267 465 470 475 480	
269 aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac	1488
270 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp	
271 485 490 495	
273 atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag	1536
274 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys	
275 500 505 510	
277 acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ctc tac agc	1584

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278	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser
279			515			520				525						
281	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	tcc	tca
282	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser
283			530			535				540						
285	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc
286	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
287	545			550			555				560					
289	ctc	tcc	ctg	tct	ccg	ggt	aaa	tga								1704
290	Leu	Ser	Leu	Ser	Pro	Gly	Lys									
291			565													
294	<210>	SEQ ID NO:	12													
295	<211>	LENGTH:	567													
296	<212>	TYPE:	PRT													
C-->	297	<213>	ORGANISM:	Artificial												
W-->	299	<220>	FEATURE:													
W-->	299	<223>	OTHER INFORMATION:	Erroneous	Field 223 requires a description	of the artificial sequence	named in field 213									
299	<400>	SEQUENCE:	12													
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302	1			5					10							15
305	Cys	Leu	Leu	Leu	Thr	Gly	Ser	Ser	Ser	Gly	Ser	Lys	Leu	Lys	Asp	Pro
306				20					25							30
309	Glu	Leu	Ser	Leu	Lys	Gly	Thr	Gln	His	Ile	Met	Gln	Ala	Gly	Gln	Thr
310				35				40								45
313	Leu	His	Leu	Gln	Cys	Arg	Gly	Glu	Ala	Ala	His	Lys	Trp	Ser	Leu	Pro
314				50				55								60
317	Glu	Met	Val	Ser	Lys	Glu	Ser	Glu	Arg	Leu	Ser	Ile	Thr	Lys	Ser	Ala
318	65				70				75							80
321	Cys	Gly	Arg	Asn	Gly	Lys	Gln	Phe	Cys	Ser	Thr	Leu	Thr	Leu	Asn	Thr
322					85				90							95
325	Ala	Gln	Ala	Asn	His	Thr	Gly	Phe	Tyr	Ser	Cys	Lys	Tyr	Leu	Ala	Val
326					100				105							110
329	Pro	Thr	Ser	Lys	Lys	Glu	Thr	Glu	Ser	Ala	Ile	Tyr	Ile	Phe	Ile	
330					115			120								125
333	Ser	Asp	Thr	Gly	Arg	Pro	Phe	Val	Glu	Met	Tyr	Ser	Glu	Ile	Pro	Glu
334					130			135								140
337	Ile	Ile	His	Met	Thr	Glu	Gly	Arg	Glu	Leu	Val	Ile	Pro	Cys	Arg	Val
338	145				150				155							160
341	Thr	Ser	Pro	Asn	Ile	Thr	Val	Thr	Leu	Lys	Lys	Phe	Pro	Leu	Asp	Thr
342					165				170							175
345	Leu	Ile	Pro	Asp	Gly	Lys	Arg	Ile	Ile	Trp	Asp	Ser	Arg	Lys	Gly	Phe
346					180				185							190
349	Ile	Ile	Ser	Asn	Ala	Thr	Tyr	Lys	Glu	Ile	Gly	Leu	Leu	Thr	Cys	Glu
350					195				200							205
353	Ala	Thr	Val	Asn	Gly	His	Leu	Tyr	Lys	Thr	Asn	Tyr	Leu	Thr	His	Arg
354					210			215								220
357	Gln	Thr	Asn	Thr	Ile	Ile	Asp	Val	Gln	Ile	Ser	Thr	Pro	Arg	Pro	Val
358	225				230				235							240
361	Lys	Leu	Leu	Arg	Gly	His	Thr	Leu	Val	Leu	Asn	Cys	Thr	Ala	Thr	Thr

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY
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DATE: 08/07/2001
TIME: 08:23:38

Input Set : A:\REG 710B.txt
Output Set: N:\CRF3\08072001\I773877.raw

L:19 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:31 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:43 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:55 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:67 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:79 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:91 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:103 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:115 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:127 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:139 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:297 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
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L:299 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:602 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
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L:879 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
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L:1002 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:1132 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
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L:1696 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
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L:1819 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:1951 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:1953 M:258 W: Mandatory Feature missing, <220> FEATURE:
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L:2204 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:2206 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:2206 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:2327 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27